

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

5' NNC AAG AGG TTN GGG GCT CTC TCC TTG TCA GTC GGC GCC GCG TGC GGG CTG GTG 54

18 27 36 45

63 72 81 90 99 108

GCT CTG TGG CAG CGG CGG CAG GAC TCC GGC ACT ATG AGC GGC TTC AGC ACC

117 126 135 144 153 162

GAG GAG CGC GCC GCG CCC TTC TCC CTG GAG TAC CGA GTC TTC CTC AAA AAT GAG

E R A A P F S L E Y R V F L K N E

171 180 189 198 207 216

AAA GGA CAA TAT ATA TCT CCA TTT CAT GAT ATT CCA ATT TAT GCA GAT AAG GAT

K G Q Y I S P F H D I P I Y A D K D

225 234 243 252 261 270

GTG TTT CAC ATG GTA GTT GAA GTA CCA CGC TGG TCT AAT GCA AAA ATG GAG ATT

V F H M V V E V P R W S N A K M E I

279 288 297 306 315 324

GCT ACA AAG GAC CCT TTA AAC CCT ATT AAA CAA GAT GTG AAA GGA AAA CTT

A T K D P L N P I K Q D V K G K L

333 342 351 360 369 378

CGC TAT GTT GCG AAT TTG TTC CCG TAT AAA GGA TAT ATC TGG AAC TAT GGT GCC

R Y V A N L F P Y K G Y I W N Y G A

FIGURE 1A

APPROVED	O.G. FIG.	
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66200T" 045T460

387	ATC CCT CAG ACT TGG GAA GAC CCA GGG CAC AAT GAT AAA CAT ACT GGC TGT TGT	432
	I P Q T W E D P G H N D K H T G C C	
396		414
405		423
432		
441	GGT GAC AAT GAC CCA ATT GAT GTG TGT GAA ATT GGA AGC AAG GTA TGT GCA AGA	486
	G D N D P I D V C E I G S K V C A R	
450		468
459		477
486		
495	GGT GAA ATA ATT GGC GTG AAA GTT CTA GGC ATA TTG GCT ATG ATT GAC GAA GGG	540
	G E I I G V K V L G I L A M I D E G	
504		522
513		531
540		
549	GAA ACC GAC TGG AAA GTC ATT GCC ATT AAT GTG GAT GAT CCT GAT GCA GCC AAT	594
	E T D W K V I A I N V D D P D A A N	
558		576
567		585
594		
603	TAT AAT GAT ATC AAT GAT GTC AAA CGG CTG AAA CCT GGC TAC TTA GAA GCT ACT	648
	Y N D I N D V K R L K P G Y L E A T	
612		630
621		639
648		
657	GTG GAC TGG TTT AGA AGG TAT AAG GTT CCT GAT GGA AAA CCA GAA AAT GAG TTT	702
	V D -W F R R Y K V P D G K P E N E F	
666		684
675		693
702		
711	GCG TTT AAT GCA GAA TTT AAA GAT AAG GAC TTT GCC ATT GAT ATT ATT AAA AGC	756
	A F N A E F K D K D F A I D I I K S	
720		738
729		747

FIGURE1B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

56200T 04521450

765	774	783	792	801	810
ACT CAT GAC CAT TGG AAA GCA TTA GTG ACT AAG AAA ACG AAT GGA AAA GGA ATC					
T H D H W K A L V T K K T N G K G I					
819	828	837	846	855	864
AGT TGC ATG AAT ACA ACT TTG TCT GAG AGC CCC TTC AAG TGT GAT CCT GAT GCT					
S C M N T T L S E S P F K C D P D A					
873	882	891	900	909	918
GCC AGA GCC ATT GTG GAT GCT TTA CCA CCA CCC TGT GAA TCT GCC TGC ACA GTA					
A R A I V D A L P P P C E S A C T V					
927	936	945	954	963	972
CCA ACA GAC GTG GAT AAG TGG TTC CAT CAC CAG AAA AAC TAA TGA GAT TTC TCT					
P T D V D K W F H H Q K N					
981	990	999	1008	1017	1026
GGA ATA CAA GCT GAT ATT GCT ACA TCG TGT TCA TCT GGA TGT ATT AGA AGT AAA					
1035	1044	1053	1062	1071	1080
AGT AGT AGC TTT TCA AAG CTT TAA ATT TGT AGA ACT CAT CTA ACT AAA GTA AAT					

FIGURE 1C

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

1089	1098	1107	1116	1125	1134
TCT GCT GTG ACT AAT CCA ATA TAC TCA GAA TGT TAT CCA TCT AAA GCA TTT TTC					
1143	1152	1161	1170	1179	1188
ATA TCT CAA CTA AGA TAA CTT TTA GCA CAT GCT TAA ATA TCA AAG CAG TTG TCA					
1197	1206	1215	1224	1233	1242
TTT GGA AGT CAC TTG TGA ATA GAT GTG CAA GGG GAG CAC ATA TTG GAT GTA TAT					
1251	1260	1269			
GTT ACC ATA TGT TAG GAA ATA AAA TTA TTT TGC TG 3'					

FIGURE 1D

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

1	MS	GFSTEE	RAAPFS	LEYRVFLKNEKGQYISPFHDIPIYAD	HPYP
1	-	-	-	-	g727225
1	MS	SFS	EERAAPFT	LEYRVFLKNEKGQYISPFHDIPIYAD	g585322
1	MT	YTT	RQIGAKNT	LEYKVIYEKD-GKPVSAFHDIPLYAD	g4199
41	KD	-	-	VFHMVVEVPRWSNAKMEIATKDP LNP I KQDVKKGKL	HPYP
1	-	-	-	-	g727225
41	KE	-	-	VFHMVVEVPRWSNAKMEIATKDP LNP I KQDVKKGKL	g585322
39	KENN	IFNMVVEI	PRWTNAKLEI	TKREET LNP I IQDTKKGKL	g4199
79	RYVANL	FPYKGYI	WNYGAI	PQTWEDPPGHNDKH TGC CGDND	HPYP
1	-	-	-	NI	g727225
79	RYVANL	FPYKGYI	WNYGAI	PQTWEDPPGHNDKH TGC CGDND	g585322
79	RFVRN	CFPHGVI	HNYGAF	PQTWEDPNVSHPE TKA VGDND	g4199
119	PIDVCE	IGSKVC	ARGEI	IGVKV L G I L A M I D E G E T D W K V I A	HPYP
37	PIDVCE	IGSKIL	SCGEV	I H V K I L G I L A L I D E G E T D W K L I A	g727225
119	PIDVCE	IGSKVC	ARGEI	I R V K V L G I L A M I D E G E T D W K V I A	g585322
119	PIDVLE	IGETIA	YTGTGQV	KQV K A L G I M A L L D E G E T D W K V I A	g4199

FIGURE 2A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

159	INVD	DDPDA	ANYND	INDV	KRL	LKPGY	LEAT	VDW	FR	YKVP	DG	HPYP
77	INAN	NDPE	ASKE	HDID	DDVK	FKPGY	LEAT	LNW	FR	LYKV	PP	g727225
159	INVE	DDPDA	ANYND	INDV	KRL	LKPGY	LEAT	VDW	FR	YKVP	DG	g585322
159	IDIN	NDPL	APKL	NDIE	DVEK	YFPGL	LRAT	NEW	FR	IYKI	IPDG	g4199
199	KPEN	EFAF	NAEF	KDKD	DFAI	DI	IKST	HDH	WKAL	VT	-KKT	NG
114												HPYP
199	KPEN	EFAF	NAEF	KDKK	NFAI	DI	IKST	HDY	WRAL	VT	-KKT	DG
199	KPEN	QFAF	SGEA	KKNK	KYAL	DI	IKST	HDY	WKQ	LI	AGKS	SDS
238	KGIS	CMNT	TLSE	SPFK	KCDP	DAAR	AI	VDAL	PPPC	-ES	ACTV	HPYP
114												g727225
238	KGIS	CMNT	TVSE	SPFQ	CDPDA	AKAI	VDAL	PPPC	-ES	ACTI		g585322
239	KGID	LTNV	TLPD	TP--	----	TYSKA	ASDA	IPPA	SLKA	DAP	I	g4199
277	PTDV	DKWF	HHQ	KN								HPYP
114												g727225
277	PTDV	DKWF	HHQ	KN								g585322
274	DKSI	DKWF	FIS	GSV								g4199

FIGURE 2B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

SEEDT DISTRO

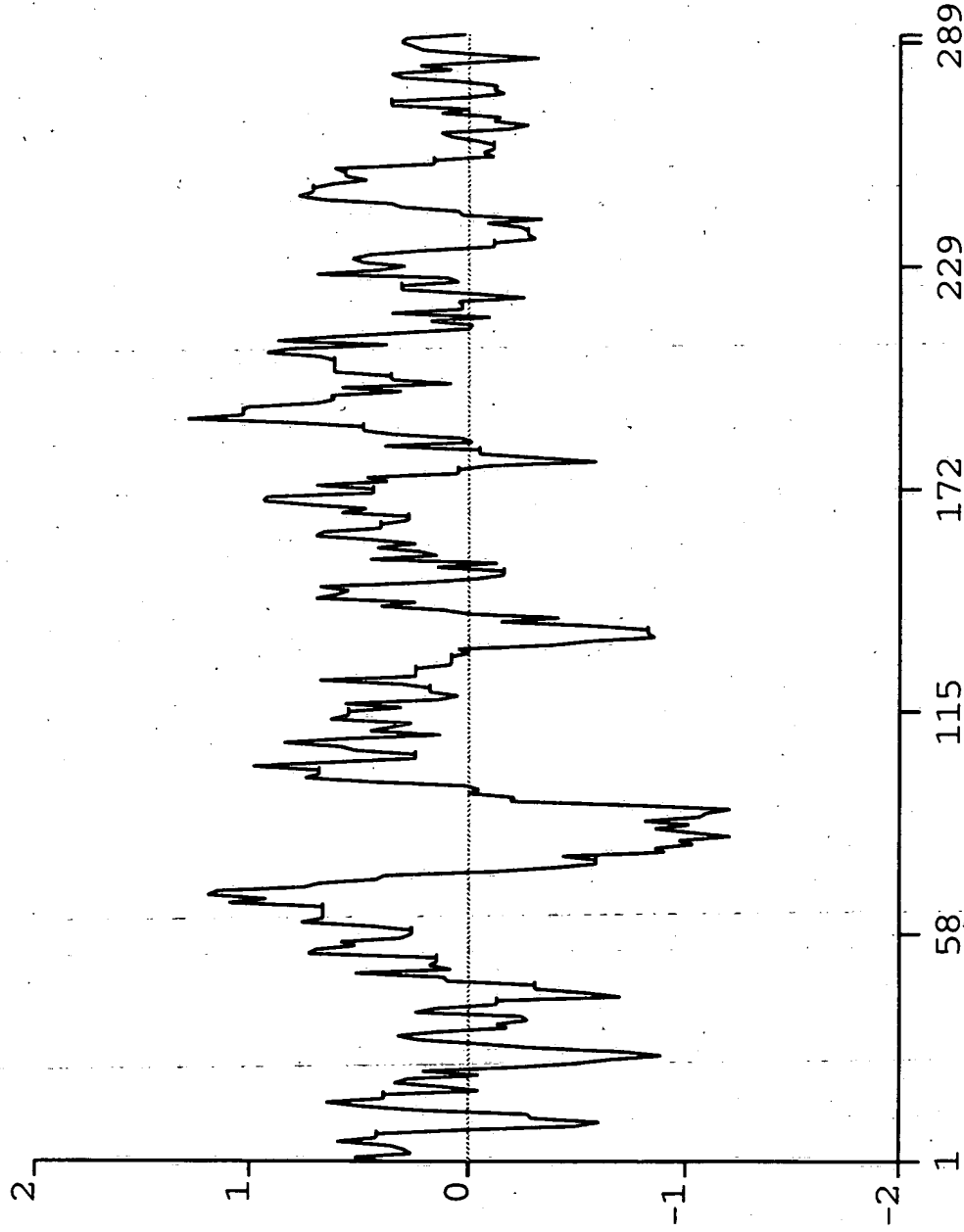


FIGURE 3

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

56200T" DISTHED

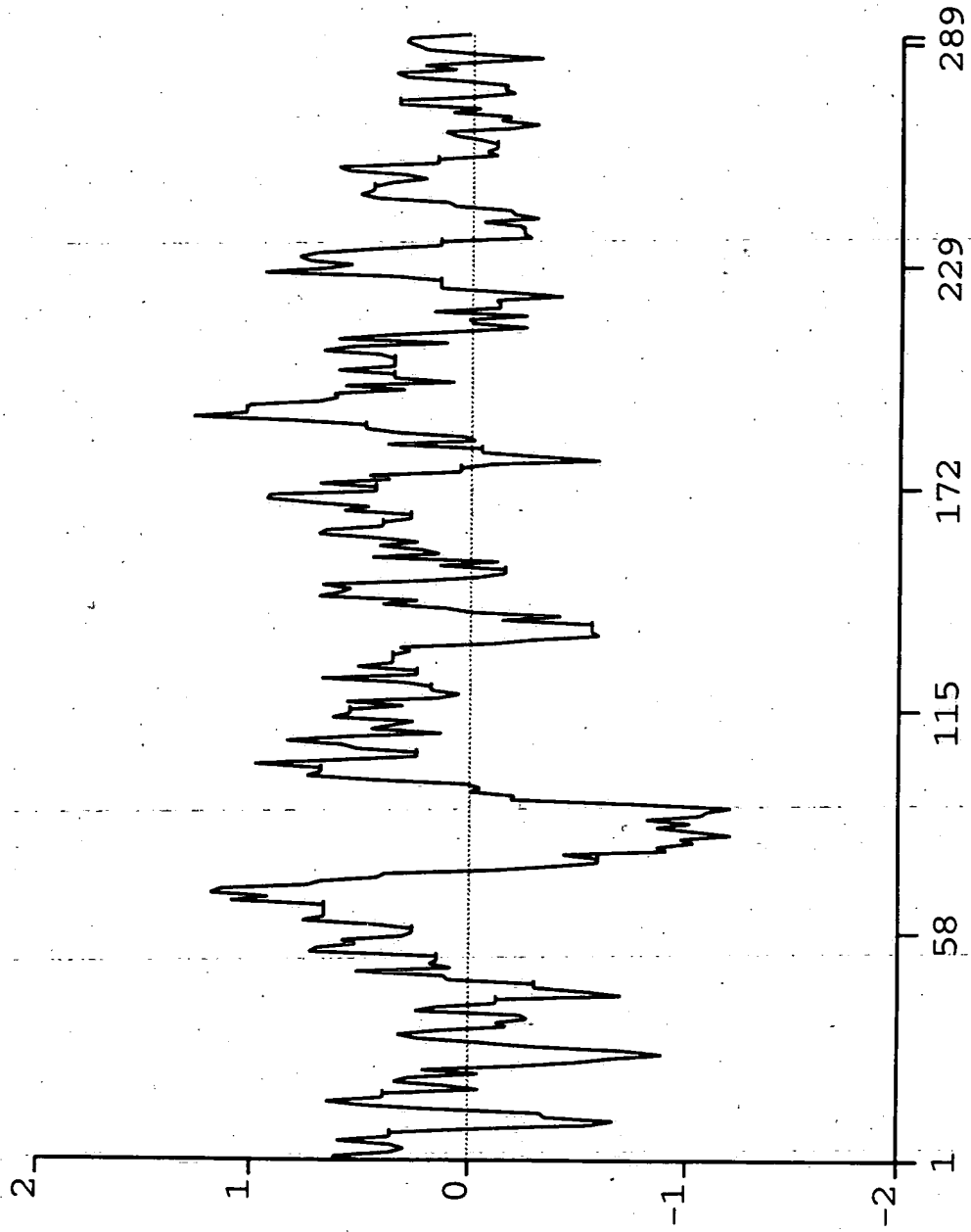


FIGURE 4

APPROVED	O.G. FIG.	
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DRAFTSMAN		

Library	Lib Description	Abun	Pct Abun
AMLENOT01	AML blast cells, blast crisis, 58 F	1	0.1049
THYRNOT01	thyroid, 64 F	3	0.0683
TBLYNOT01	T-B lymphoblast cell line, leukemia	2	0.0651
COLANTUT03	colon tumor, 62 M, match to COLANOT16	2	0.0543
U937NOT01	U937 monocyte cell line, 37 M	1	0.0495
TESTNOT01	testis, 37 M	1	0.0469
HNT2AGT01	hNT-2 cell line, post-mitotic neurons	2	0.0380
PROSTUT03	prostate tumor, 67 M, match to PROSNOT05	1	0.0351
LVENNOT03	heart, left ventricle, 31 M	1	0.0336
BRSTNOT03	breast, 54 F, match to BRSTTUT02	2	0.0293
PANCRNOT07	pancreas, fetal M	1	0.0286
BEPINON01	bronchial epithelium, primary cell line, 54 M, NORM	1	0.0273
PANCTUT01	pancreatic tumor, 65 F, match to PANCNOT08	1	0.0257
MENITUT03	brain tumor, benign meningioma, 35 F	1	0.0249
TMLR3DT01	lymphocytes (non-adher PBMC), M, 96-hr MLR	1	0.0228
COLANTUT02	colon tumor, 75 M, match to COLANOT01	1	0.0220
SYNORAB01	synovium, hip, rheumatoid, 68 F	1	0.0194
LUNGNOT04	lung, 2 M	1	0.0182
SYNORAT04	synovium, wrist, rheumatoid, 62 F	1	0.0173
NGANNOT01	ganglioneuroma, 9 M	1	0.0155
BRSTNOT05	breast, 58 F, match to BRSTTUT03	1	0.0154

FIGURE 5